Influence of microbial diversity on carbon use efficiency in soils

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Goals:

1. To develop a soil model system in which microbial communities and abiotic conditions can be manipulated
2. Quantify the relative importance of biotic and abiotic drivers of CUE

Abstract:

Soils retain the largest organic carbon pool in the terrestrial biosphere and represent an important source of carbon dioxide (CO_2) to the atmosphere. Microbial carbon use efficiency (CUE) – or the fraction of C taken up by a cell that is converted to biomass – is a central determinant of how much of this carbon is able to be retained in soil. CUE has been proposed to vary with both biotic and abiotic conditions. Therefore, understanding how this pivotal variable in the C cycle will respond to the dually changing climate and biodiversity is of utmost importance. The present study addresses how microbial diversity, community composition, rising temperatures and different moisture impact CUE and its consequences for soil CO_2 fluxes.

Here, we extracted communities exposed to chronic warming and ambient temperature controls from a long-term experimental site at the Harvard Forest. The diversity of these communities was manipulated prior to inoculation in an artificial soil environment. Microcosms were incubated for 120 days under two temperatures and moistures. Subsequently ^{18}O-H_2O was added and CUE was evaluated after microbes were growing for 24h. The diversity of bacteria and fungi was determined by Illumina MiSeq. Because there was no observed difference in CUE that could be attributed to long-term warming treatment, this factor was dropped from the analysis, though it was maintained in the experiments.

Overall, more diverse treatments showed higher CUE compared to less diverse treatments. The greatest difference in CUE was observed between microcosms containing bacteria and those containing both bacteria and fungi, where microcosms with fungi had higher CUE compared to those without. Moisture and incubation temperature influenced the bacterial and fungal microbial communities. Moreover, moisture was a stronger predictor of communities than temperature, explaining 7.9% and 2.5% of bacterial community structure, respectively. CUE decreased in response to increasing temperature from 15 to 25°C, ranging from -0.03 to +0.008 $^{o}C^{-1}$. Decreasing moisture from 60 to 30% water holding capacity mostly decreased CUE to up to 56%. Bacterial community structure explained the highest fraction of variance in CUE (25%), while moisture and temperature explain both less than 1%. Fungal alpha and beta diversity showed a minor influence on CUE. This could be due to a slower growth of fungi compared to

bacteria which has not been captured by the relatively short incubation time for the CUE ^{18}O-H_2O method. We showed that moisture, a factor that has been overlooked in many CUE studies, was important to understand microbial CUE. Altogether, these results lay the foundation for a better understanding on how microbial community composition and abiotic factors may interact to drive changes in soil carbon cycling.

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